



SEQUENCE LISTING

<110> Jensen, Michael

<120> Selection Systems for Genetically Modified Cells

<130> 24751-2502

<140> US/09/846,637

<141> 2001-04-30

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<222> (48)...(1589)

<223> Human Wild-type Inosine Monophosphate Dehydrogenase II (IMPDH II)

<300>

<301> Collart, F.R. and Huberman, E.

<302> Cloning and sequence analysis of the human and

<303> J. Biol. Chem. (1988)

<304> 263

<306> 15769-15772

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aattc

1654

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 <303> J. Biol. Chem. (1997)
 <304> 272
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<302> Isolation and Characterization of Mycophenolic
<303> J. Biol. Chem. (1997)
<304> 272
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 <301> Farazi et al.
 <303> J. Biol. Chem. (1997)
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Gly Leu Val Thr Gln Arg Asp Tyr Pro Ile Asp Leu Thr Gln Thr Glu	
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Thr Lys Val Ser Asp Met Met Thr Pro Phe Ser Lys Leu Val Thr Ala	
165 170 175	
His Gln Asp Thr Lys Leu Ser Glu Ala Asn Lys Ile Ile Trp Glu Lys	
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Lys Leu Asn Ala Leu Pro Ile Ile Asp Asp Asp Gln His Leu Arg Tyr	
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Ile Val Phe Arg Lys Asp Tyr Asp Arg Ser Gln Val Cys His Asn Glu	
210 215 220	
Leu Val Asp Ser Gln Lys Arg Tyr Leu Val Gly Ala Gly Ile Asn Thr	
225 230 235 240	
Arg Asp Phe Arg Glu Arg Val Pro Ala Leu Val Glu Ala Gly Ala Asp	
245 250 255	
Val Leu Cys Ile Asp Ser Ser Asp Gly Phe Ser Glu Trp Gln Lys Ile	
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Thr Ile Gly Trp Ile Arg Glu Lys Tyr Gly Asp Lys Val Lys Val Gly	
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Ala Gly Asn Ile Val Asp Gly Glu Gly Phe Arg Tyr Leu Ala Asp Ala	

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Thr	Arg	Glu	Gln	Lys	Gly	Ile	Gly	Arg	Gly	Gln	Ala	Thr	Ala	Val	Ile
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Asp	Val	Val	Ala	Glu	Arg	Asn	Lys	Tyr	Phe	Glu	Glu	Thr	Gly	Ile	Tyr
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Ile	Pro	Val	Cys	Ser	Asp	Gly	Gly	Ile	Val	Tyr	Asp	Tyr	His	Met	Thr
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Leu	Ala	Leu	Ala	Met	Gly	Ala	Asp	Phe	Ile	Met	Leu	Gly	Arg	Tyr	Phe
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Val	Met	Lys	Glu	Tyr	Trp	Gly	Glu	Gly	Ser	Ser	Arg	Ala	Arg	Asn	Trp
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Gln	Arg	Tyr	Asp	Leu	Gly	Gly	Lys	Gln	Lys	Leu	Ser	Phe	Glu	Glu	Gly
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Val	Asp	Ser	Tyr	Val	Pro	Tyr	Ala	Gly	Lys	Leu	Lys	Asp	Asn	Val	Glu
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Ala	Ser	Leu	Asn	Lys	Val	Lys	Ser	Thr	Met	Cys	Asn	Cys	Gly	Ala	Leu
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Val	Ser	Ile	Val	Glu	Gly	Gly	Ala	His	Asp	Val	Ile	Val	Lys	Asp	Arg
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Leu Gly Gly Cys Arg Arg Leu Pro Leu Thr Cys Arg Gln Leu Arg Phe	
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gcc tcc gac agc gga gcc gca gcg gca act aca aaa gca acg gcc gaa	144
Ala Ser Asp Ser Gly Ala Ala Ala Thr Thr Lys Ala Thr Ala Glu	
35 40 45	
tca gca gcc gag tca gct agt ata aac gtc aaa gag gca ccc aaa aag	192
Ser Ala Ala Glu Ser Ala Ser Ile Asn Val Lys Glu Ala Pro Lys Lys	
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gcc gga cgg ggc ctg cgg cgc acg gtc ctg gga acg tcg ttg gcg ctg	240
Ala Gly Arg Gly Leu Arg Arg Thr Val Leu Gly Thr Ser Leu Ala Leu	
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acg ctg ctg gtt gga tat gtc tac ggg acg gac acc cgg gcg agt gtg	288
Thr Leu Leu Val Gly Tyr Val Tyr Gly Thr Asp Thr Arg Ala Ser Val	
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cat cgg tac ggt gtt gtg ccg ctg att aga gca ttg tat cct gat gcg	336
His Arg Tyr Gly Val Val Pro Leu Ile Arg Ala Leu Tyr Pro Asp Ala	
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gaa gat gcg cat cat att ggt gtc gat act tta aag atg ctg tat aag	384
Glu Asp Ala His His Ile Gly Val Asp Thr Leu Lys Met Leu Tyr Lys	
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Tyr Gly Leu His Pro Arg Glu Arg Gly Asp Pro Asp Gly Asp Gly Ala	
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Leu Ala Thr Glu Val Phe Gly Tyr Thr Leu Ser Asn Pro Ile Gly Ile	
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Ser Gly Gly Leu Asp Lys His Ala Glu Ile Pro Asp Pro Leu Phe Ala	
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Ile Gly Pro Ala Ile Val Glu Val Gly Gly Thr Thr Pro Leu Pro Gln	
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Asp Gly Asn Pro Arg Pro Arg Val Phe Arg Leu Pro Ser Gln Arg Ala	
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Met Ile Asn Arg Tyr Gly Leu Asn Ser Lys Gly Ala Asp His Met Ala	
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Ala Ile Leu Glu Gln Arg Val Arg Asp Phe Ala Tyr Ala Asn Gly Phe	
225 230 235 240	
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Gly Ala Tyr Asp Ala Ala Lys Gln Arg Val Leu Asp Gly Glu Ala Gly	
245 250 255	
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Val Pro Pro Gly Ser Leu Gln Pro Gly Lys Leu Leu Ala Val Gln Val	
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gca aag aac aag gcc act cct gac ggc gac att gaa gcc atc aag cgc	864
Ala Lys Asn Lys Ala Thr Pro Asp Gly Asp Ile Glu Ala Ile Lys Arg	
275 280 285	
gac tat gtg tat tgc gtg gac cgt gtg gcc aaa tac gct gat att ctt	912
Asp Tyr Val Tyr Cys Val Asp Arg Val Ala Lys Tyr Ala Asp Ile Leu	
290 295 300	
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Val Val Asn Val Ser Ser Pro Asn Thr Pro Gly Leu Arg Asp Leu Gln	
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gcc act gcc ccg ctc aca gct atc ttg agt gct gtc gtt ggc gcg gca	1008
Ala Thr Ala Pro Leu Thr Ala Ile Leu Ser Ala Val Val Gly Ala Ala	
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Lys Ser Val Asn Arg Lys Thr Lys Pro Tyr Val Met Val Lys Val Ser	
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Pro Asp Glu Asp Ser Asp Glu Gln Val Ser Gly Ile Cys Asp Ala Val	
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Arg Ala Ser Gly Val Asp Gly Val Ile Val Gly Asn Thr Thr Asn Arg	
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Arg Pro Asp Pro Ile Pro Gln Gly Tyr Thr Leu Pro Ala Lys Glu Gln	
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Ala Thr Leu Lys Glu Thr Gly Gly Tyr Ser Gly Pro Gln Leu Phe Asp	
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cgc aca gtg gcc ctt gtg gct cgg tac cgc tcc atg ctg gat gcg gag	1296
Arg Thr Val Ala Leu Val Ala Arg Tyr Arg Ser Met Leu Asp Ala Glu	
420 425 430	
tcg gaa acg gcc gga tcc gcc aag gat tca gca gcg acc ata gcg caa	1344
Ser Glu Thr Ala Gly Ser Ala Lys Asp Ser Ala Ala Thr Ile Ala Gln	
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aca gag cca ggc tcg gaa aac gtt cct cct gtg gaa gcg cca agc gga	1392
Thr Glu Pro Gly Ser Glu Asn Val Pro Pro Val Glu Ala Pro Ser Gly	
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Leu Pro Arg Lys Val Ile Phe Ala Ser Gly Gly Ile Thr Asn Gly Lys	
465 470 475 480	
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Gln Ala His Ala Val Leu Asp Thr Gly Ala Ser Val Ala Met Met Tyr	
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acc ggt gtg gtc tat ggt ggc gtc ggc act gtc act cga gtg aag caa	1536
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Glu Leu Arg Thr Ala Lys Lys Glu	
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Ser Ala Ala Glu Ser Ala Ser Ile Asn Val Lys Glu Ala Pro Lys Lys	
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Ala Gly Arg Gly Leu Arg Arg Thr Val Leu Gly Thr Ser Leu Ala Leu	
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Thr Leu Leu Val Gly Tyr Val Tyr Gly Thr Asp Thr Arg Ala Ser Val	
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His Arg Tyr Gly Val Val Pro Leu Ile Arg Ala Leu Tyr Pro Asp Ala	
100 105 110	
Glu Asp Ala His His Ile Gly Val Asp Thr Leu Lys Met Leu Tyr Lys	
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Tyr Gly Leu His Pro Arg Glu Arg Gly Asp Pro Asp Gly Asp Gly Ala	
130 135 140	
Leu Ala Thr Glu Val Phe Gly Tyr Thr Leu Ser Asn Pro Ile Gly Ile	
145 150 155 160	
Ser Gly Gly Leu Asp Lys His Ala Glu Ile Pro Asp Pro Leu Phe Ala	
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Ile Gly Pro Ala Ile Val Glu Val Gly Gly Thr Thr Pro Leu Pro Gln	

180 185 190
 Asp Gly Asn Pro Arg Pro Arg Val Phe Arg Leu Pro Ser Gln Arg Ala
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 Met Ile Asn Arg Tyr Gly Leu Asn Ser Lys Gly Ala Asp His Met Ala
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 225 230 235 240
 Gly Ala Tyr Asp Ala Ala Lys Gln Arg Val Leu Asp Gly Glu Ala Gly
 245 250 255
 Val Pro Pro Gly Ser Leu Gln Pro Gly Lys Leu Leu Ala Val Gln Val
 260 265 270
 Ala Lys Asn Lys Ala Thr Pro Asp Gly Asp Ile Glu Ala Ile Lys Arg
 275 280 285
 Asp Tyr Val Tyr Cys Val Asp Arg Val Ala Lys Tyr Ala Asp Ile Leu
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 Val Val Asn Val Ser Ser Pro Asn Thr Pro Gly Leu Arg Asp Leu Gln
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 Pro Asp Glu Asp Ser Asp Glu Gln Val Ser Gly Ile Cys Asp Ala Val
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 Arg Ala Ser Gly Val Asp Gly Val Ile Val Gly Asn Thr Thr Asn Arg
 370 375 380
 Arg Pro Asp Pro Ile Pro Gln Gly Tyr Thr Leu Pro Ala Lys Glu Gln
 385 390 395 400
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 405 410 415
 Arg Thr Val Ala Leu Val Ala Arg Tyr Arg Ser Met Leu Asp Ala Glu
 420 425 430
 Ser Glu Thr Ala Gly Ser Ala Lys Asp Ser Ala Ala Thr Ile Ala Gln
 435 440 445
 Thr Glu Pro Gly Ser Glu Asn Val Pro Pro Val Glu Ala Pro Ser Gly
 450 455 460
 Leu Pro Arg Lys Val Ile Phe Ala Ser Gly Gly Ile Thr Asn Gly Lys
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 Gln Ala His Ala Val Leu Asp Thr Gly Ala Ser Val Ala Met Met Tyr
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 <301> Natsumeda et al.
 <302> Two Distinct cDNAs for Human IMP Dehydrogenase
 <303> J. Biol. Chem. (1990)
 <304> 265
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 ctgggatggg agagacgaac cgagtctagg catctgcgta gcagcgccgg ggagagcggg 180
 gagcccaggc ggagcccagt cgactcccgg attcccctgc cccgcccccg gcacgaggcc 240

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cactccacca	ccgctgcagg	gaggcggacg	gcgctgttcc	ggagcccgga	gcccggcaac	420
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atg gcg gac	tac ctg atc	agc ggc ggc	acc ggc	tac gtg ccc	gag gat	648
Met Ala Asp	Tyr Leu Ile	Ser Gly Gly	Thr Gly Tyr	Val Pro	Glu Asp	
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Gly Leu Thr	Ala Gln Gln	Leu Phe	Ala Ser	Ala Asp	Asp Leu	
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aac gac ttc	ctg att ctc	cca gga ttc	ata gac ttc	ata gct gat	gag	744
Asn Asp Phe	Leu Ile Leu	Pro Gly Phe	Ile Asp Phe	Ile Ala Asp	Glu	
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gtg gac ctg	acc tca gcc	ctg acc cgg	aag atc acg	ctg aag acg	cca	792
Val Asp Leu	Thr Ser Ala	Leu Thr Arg	Lys Ile Thr	Leu Lys Thr	Pro	
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ctc atc tcc	tcc ccc atg	gac act gtg	aca gag gct	gac atg gcc	att	840
Leu Ile Ser	Ser Pro Met	Asp Thr Val	Thr Glu Ala	Asp Met Ala	Ile	
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gcc atg gct	ctg atg gga	ggt att ggg	ttc att cac	cac aac tgc	acc	888
Ala Met Ala	Leu Met Gly	Gly Ile Gly	Phe Ile His	His Asn Cys	Thr	
	85	90		95		
cca gag ttc	cag gcc aat	gaa gta cgc	aag gtc aag	aac ttt gaa	cag	936
Pro Glu Phe	Gln Ala Asn	Glu Val Arg	Lys Val Lys	Asn Phe Glu	Gln	
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ggc ttc atc	acg gac cct	gtg gtg ctg	agc ccc tcg	cac act gtg	ggc	984
Gly Phe Ile	Thr Asp Pro	Val Leu Ser	Pro Ser Ser	His Thr Val	Gly	
	115	120		125		
gat gtg ctg	gag gcc aag	atg cgg cat	ggc ttc tct	ggc atc ccc	atc	1032
Asp Val Leu	Glu Ala Lys	Met Arg His	Gly Phe Ser	Gly Ile Pro	Ile	
	130	135		140		
act gag acg	ggc acc atg	ggc agc aag	ctg gtg ggc	atc gtc acc	tcc	1080
Thr Glu Thr	Gly Thr Met	Gly Ser Lys	Leu Val Gly	Ile Val Thr	Ser	
	145	150		155	160	
cga gac atc	gac ttt ctt	gct gag aag	gac cac acc	acc acc ctc	ctc agt	1128
Arg Asp Ile	Asp Phe Leu	Ala Glu Lys	Asp His Thr	Thr Thr Leu	Leu Ser	
	165	170		175		
gag gtg atg	acg cca agg	att gaa ctg	gtg gtg gct	cca gca ggt	gtg	1176
Glu Val Met	Thr Pro Arg	Ile Glu Leu	Val Val Ala	Pro Ala Gly	Val	
	180	185		190		
acg ttg aaa	gag gca aat	gag atc ctg	cag cgt agc	aag aaa ggg	aag	1224
Thr Leu Lys	Glu Ala Asn	Glu Ile Leu	Gln Arg Ser	Lys Lys Gly	Lys	
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ctg cct atc	gtc aat gat	tgc gat gag	ctg gtg gcc	atc atc gcc	cgc	1272
Leu Pro Ile	Val Asn Asp	Cys Asp Glu	Leu Val Ala	Ile Ile Ala	Arg	
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acc gac ctg	aag aag aat	cga gac tac	cct ctg gcc	tcc aag gat	tcc	1320
Thr Asp Leu	Lys Lys Asn	Arg Asp Tyr	Pro Leu Ala	Ser Lys Asp	Ser	
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cag aag cag	ctg ctc tgt	ggg gca gct	gtg ggc acc	cgt gag gat	gac	1368

Gln	Lys	Gln	Leu	Leu	Cys	Gly	Ala	Ala	Val	Gly	Thr	Arg	Glu	Asp	Asp	
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Lys	Tyr	Arg	Leu	Asp	Leu	Leu	Thr	Gln	Ala	Gly	Val	Asp	Val	Ile	Val	
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Phe	His	Ser	Ser	Gln	Gly	Asn	Ser	Val	Tyr	Gln	Ile	Ala	Met	Val	His	
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tac	atc	aaa	cag	aag	tac	ccc	cac	ctc	cag	gtg	att	ggg	ggg	aac	gtg	1512
Tyr	Ile	Lys	Gln	Lys	Tyr	Pro	His	Leu	Gln	Val	Ile	Gly	Gly	Asn	Val	
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Val	Thr	Ala	Ala	Gln	Ala	Lys	Asn	Leu	Ile	Asp	Ala	Gly	Val	Asp	Gly	
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ctg	cgc	gtg	ggc	atg	ggc	tgc	ggc	tcc	atc	tgc	atc	acc	cag	gaa	gtg	1608
Leu	Arg	Val	Gly	Met	Gly	Cys	Gly	Ser	Ile	Cys	Ile	Thr	Gln	Glu	Val	
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Met	Ala	Cys	Gly	Arg	Pro	Gln	Gly	Thr	Ala	Val	Tyr	Lys	Val	Ala	Glu	
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Tyr	Ala	Arg	Arg	Phe	Gly	Val	Pro	Ile	Ile	Ala	Asp	Gly	Gly	Ile	Gln	
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acc	gtg	gga	cac	gtg	gtc	aag	gcc	ctg	gcc	ctt	gga	gcc	tcc	aca	gtg	1752
Thr	Val	Gly	His	Val	Val	Lys	Ala	Leu	Ala	Leu	Gly	Ala	Ser	Thr	Val	
	370					375					380					
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Met	Met	Gly	Ser	Leu	Leu	Ala	Ala	Thr	Thr	Glu	Ala	Pro	Gly	Glu	Tyr	
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Phe	Phe	Ser	Asp	Gly	Val	Arg	Leu	Lys	Lys	Tyr	Arg	Gly	Met	Gly	Ser	
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ctg	gat	ccc	atg	gag	aag	agc	agc	agc	agc	cag	aaa	cga	tac	ttc	agc	1896
Leu	Asp	Pro	Met	Glu	Lys	Ser	Ser	Ser	Ser	Gln	Lys	Arg	Tyr	Phe	Ser	
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Glu	Gly	Asp	Lys	Val	Lys	Ile	Ala	Gln	Gly	Val	Ser	Gly	Ser	Ile	Gln	
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Asp	Lys	Gly	Ser	Ile	Gln	Lys	Phe	Val	Pro	Tyr	Leu	Ile	Ala	Gly	Ile	
	450					455					460					
caa	cac	ggc	tgc	cag	gat	atc	ggg	gcc	cgc	agc	ctg	tct	gtc	ctt	cgg	2040
Gln	His	Gly	Cys	Gln	Asp	Ile	Gly	Ala	Arg	Ser	Leu	Ser	Val	Leu	Arg	
465					470					475					480	
tcc	atg	atg	tac	tca	gga	gag	ctc	aag	ttt	gag	aag	cgg	acc	atg	tcg	2088
Ser	Met	Met	Tyr	Ser	Gly	Glu	Leu	Lys	Phe	Glu	Lys	Arg	Thr	Met	Ser	
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ccc	cag	att	gag	ggg	ggg	gtc	cat	ggc	ctg	cac	tct	tac	gaa	aag	cgg	2136
Pro	Gln	Ile	Glu	Gly	Gly	Val	His	Gly	Leu	His	Ser	Tyr	Glu	Lys	Arg	
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Leu Tyr

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gcaggt 2858

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<211> 514
<212> PRT
<213> Homo sapien

<400> 18

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			20					25					30		
Asn	Asp	Phe	Leu	Ile	Leu	Pro	Gly	Phe	Ile	Asp	Phe	Ile	Ala	Asp	Glu
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Val	Asp	Leu	Thr	Ser	Ala	Leu	Thr	Arg	Lys	Ile	Thr	Leu	Lys	Thr	Pro
	50					55					60				
Leu	Ile	Ser	Ser	Pro	Met	Asp	Thr	Val	Thr	Glu	Ala	Asp	Met	Ala	Ile
65					70					75					80
Ala	Met	Ala	Leu	Met	Gly	Gly	Ile	Gly	Phe	Ile	His	His	Asn	Cys	Thr
			85					90					95		
Pro	Glu	Phe	Gln	Ala	Asn	Glu	Val	Arg	Lys	Val	Lys	Asn	Phe	Glu	Gln
			100					105					110		
Gly	Phe	Ile	Thr	Asp	Pro	Val	Val	Leu	Ser	Pro	Ser	His	Thr	Val	Gly
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Asp	Val	Leu	Glu	Ala	Lys	Met	Arg	His	Gly	Phe	Ser	Gly	Ile	Pro	Ile
	130					135					140				
Thr	Glu	Thr	Gly	Thr	Met	Gly	Ser	Lys	Leu	Val	Gly	Ile	Val	Thr	Ser
145					150					155					160
Arg	Asp	Ile	Asp	Phe	Leu	Ala	Glu	Lys	Asp	His	Thr	Thr	Leu	Leu	Ser
			165					170					175		
Glu	Val	Met	Thr	Pro	Arg	Ile	Glu	Leu	Val	Val	Ala	Pro	Ala	Gly	Val
			180				185						190		
Thr	Leu	Lys	Glu	Ala	Asn	Glu	Ile	Leu	Gln	Arg	Ser	Lys	Lys	Gly	Lys
		195				200						205			
Leu	Pro	Ile	Val	Asn	Asp	Cys	Asp	Glu	Leu	Val	Ala	Ile	Ile	Ala	Arg
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Thr	Asp	Leu	Lys	Lys	Asn	Arg	Asp	Tyr	Pro	Leu	Ala	Ser	Lys	Asp	Ser
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Gln	Lys	Gln	Leu	Leu	Cys	Gly	Ala	Ala	Val	Gly	Thr	Arg	Glu	Asp	Asp
			245					250						255	
Lys	Tyr	Arg	Leu	Asp	Leu	Leu	Thr	Gln	Ala	Gly	Val	Asp	Val	Ile	Val
			260				265						270		
Phe	His	Ser	Ser	Gln	Gly	Asn	Ser	Val	Tyr	Gln	Ile	Ala	Met	Val	His
		275				280						285			
Tyr	Ile	Lys	Gln	Lys	Tyr	Pro	His	Leu	Gln	Val	Ile	Gly	Gly	Asn	Val
	290					295					300				
Val	Thr	Ala	Ala	Gln	Ala	Lys	Asn	Leu	Ile	Asp	Ala	Gly	Val	Asp	Gly
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Leu	Arg	Val	Gly	Met	Gly	Cys	Gly	Ser	Ile	Cys	Ile	Thr	Gln	Glu	Val
			325					330					335		
Met	Ala	Cys	Gly	Arg	Pro	Gln	Gly	Thr	Ala	Val	Tyr	Lys	Val	Ala	Glu
			340					345					350		

Tyr Ala Arg Arg Phe Gly Val Pro Ile Ile Ala Asp Gly Gly Ile Gln
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 Thr Val Gly His Val Val Lys Ala Leu Ala Leu Gly Ala Ser Thr Val
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 Met Met Gly Ser Leu Leu Ala Ala Thr Thr Glu Ala Pro Gly Glu Tyr
 385 390 395 400
 Phe Phe Ser Asp Gly Val Arg Leu Lys Lys Tyr Arg Gly Met Gly Ser
 405 410 415
 Leu Asp Pro Met Glu Lys Ser Ser Ser Ser Gln Lys Arg Tyr Phe Ser
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 Glu Gly Asp Lys Val Lys Ile Ala Gln Gly Val Ser Gly Ser Ile Gln
 435 440 445
 Asp Lys Gly Ser Ile Gln Lys Phe Val Pro Tyr Leu Ile Ala Gly Ile
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 Gln His Gly Cys Gln Asp Ile Gly Ala Arg Ser Leu Ser Val Leu Arg
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 <223> Human wild-type Dihydroorotate Dehydrogenase
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 <300>
 <301> Minet, M., Dufour, M-E., and Lacroute, F.
 <302> Cloning and Sequencing of a Human cDNA coding for
 <303> Gene (1992)
 <304> 121
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 Ile Leu Gly Gly Gly Gly Leu Leu Phe Ala Ser Tyr Leu Met Ala Thr
 20 25 30

 gga gat gag cgt ttc tat gct gaa cac ctg atg ccg act ctg cag ggg 144
 Gly Asp Glu Arg Phe Tyr Ala Glu His Leu Met Pro Thr Leu Gln Gly
 35 40 45

 ctg ctg gac ccg gag tca gcc cac aga ctg gct gtt cgc ttc acc tcc 192
 Leu Leu Asp Pro Glu Ser Ala His Arg Leu Ala Val Arg Phe Thr Ser
 50 55 60

 ctg ggg ctc ctt cca cgg gcc aga ttt caa gac tct gac atg ctg gaa 240
 Leu Gly Leu Leu Pro Arg Ala Arg Phe Gln Asp Ser Asp Met Leu Glu
 65 70 75 80

 gtg aga gtt ctg ggc cat aaa ttc cga aat cca gta gga att gct gca 288
 Val Arg Val Leu Gly His Lys Phe Arg Asn Pro Val Gly Ile Ala Ala
 85 90 95

 gga ttt gac aag cat ggg gaa gcc gtg gac gga ctt tat aag atg ggc 336

Gly	Phe	Asp	Lys	His	Gly	Glu	Ala	Val	Asp	Gly	Leu	Tyr	Lys	Met	Gly	
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Phe	Gly	Phe	Val	Glu	Ile	Gly	Ser	Val	Thr	Pro	Lys	Pro	Gln	Glu	Gly	
		115					120					125				
aac	cct	aga	ccc	aga	gtc	ttc	cgc	ctc	cct	gag	gac	caa	gct	gtc	att	432
Asn	Pro	Arg	Pro	Arg	Val	Phe	Arg	Leu	Pro	Glu	Asp	Gln	Ala	Val	Ile	
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Asn	Arg	Tyr	Gly	Phe	Asn	Ser	His	Gly	Leu	Ser	Val	Val	Glu	His	Arg	
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Leu	Arg	Ala	Arg	Gln	Gln	Lys	Gln	Ala	Lys	Leu	Thr	Glu	Asp	Gly	Leu	
				165					170					175		
cct	ctg	ggg	gtc	aac	ttg	ggg	aag	aac	aag	acc	tca	gtg	gac	gcc	gcg	576
Pro	Leu	Gly	Val	Asn	Leu	Gly	Lys	Asn	Lys	Thr	Ser	Val	Asp	Ala	Ala	
			180					185					190			
gag	gac	tac	gca	gaa	ggg	gtg	cgc	gta	ctg	ggc	ccc	ctg	gcc	gac	tac	624
Glu	Asp	Tyr	Ala	Glu	Gly	Val	Arg	Val	Leu	Gly	Pro	Leu	Ala	Asp	Tyr	
		195					200					205				
ctg	gtg	gtg	aat	gtg	tcc	agc	ccc	aac	act	gcc	ggg	ctg	cgg	agc	ctt	672
Leu	Val	Val	Asn	Val	Ser	Ser	Pro	Asn	Thr	Ala	Gly	Leu	Arg	Ser	Leu	
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Gln	Gly	Lys	Ala	Glu	Leu	Arg	Arg	Leu	Leu	Thr	Lys	Val	Leu	Gln	Glu	
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Arg	Asp	Gly	Leu	Arg	Arg	Val	His	Arg	Pro	Ala	Val	Leu	Val	Lys	Ile	
				245					250					255		
gct	cct	gac	ctc	acc	agc	cag	gat	aag	gag	gac	att	gcc	agt	gtg	gtc	816
Ala	Pro	Asp	Leu	Thr	Ser	Gln	Asp	Lys	Glu	Asp	Ile	Ala	Ser	Val	Val	
			260					265					270			
aaa	gag	ttg	ggc	atc	gat	ggg	ctg	att	gtt	acg	aac	acc	acc	gtg	agt	864
Lys	Glu	Leu	Gly	Ile	Asp	Gly	Leu	Ile	Val	Thr	Asn	Thr	Thr	Val	Ser	
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Arg	Pro	Ala	Gly	Leu	Gln	Gly	Ala	Leu	Arg	Ser	Glu	Thr	Gly	Gly	Leu	
	290					295					300					
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Ser	Gly	Lys	Pro	Leu	Arg	Asp	Leu	Ser	Thr	Gln	Thr	Ile	Arg	Glu	Met	
	305				310					315					320	
tat	gca	ctc	acc	caa	ggc	cga	gtt	ccc	ata	att	ggg	gtt	ggt	ggt	gtg	1008
Tyr	Ala	Leu	Thr	Gln	Gly	Arg	Val	Pro	Ile	Ile	Gly	Val	Gly	Gly	Val	
				325					330					335		
agc	agc	ggg	cag	gac	gcg	ctg	gag	aag	atc	cgg	gca	ggg	gcc	tcc	ctg	1056
Ser	Ser	Gly	Gln	Asp	Ala	Leu	Glu	Lys	Ile	Arg	Ala	Gly	Ala	Ser	Leu	
			340					345					350			
gtg	cag	ctg	tac	acg	gcc	ctc	acc	ttc	tgg	ggg	cca	ccc	gtt	gtg	ggc	1104
Val	Gln	Leu	Tyr	Thr	Ala	Leu	Thr	Phe	Trp	Gly	Pro	Pro	Val	Val	Gly	
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 Lys Val Lys Arg Glu Leu Glu Ala Leu Leu Lys Glu Gln Gly Phe Gly
 370 375 380

gga gtc aca gat gcc att gga gca gat cat cgg agg tgaggacagc 1198
 Gly Val Thr Asp Ala Ile Gly Ala Asp His Arg Arg
 385 390 395

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 ccataaactg catttttgat tctttgtgga ttcaaaccct aggatccatc agtcttgcaa 1438
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 35 40 45
 Leu Leu Asp Pro Glu Ser Ala His Arg Leu Ala Val Arg Phe Thr Ser
 50 55 60
 Leu Gly Leu Leu Pro Arg Ala Arg Phe Gln Asp Ser Asp Met Leu Glu
 65 70 75 80
 Val Arg Val Leu Gly His Lys Phe Arg Asn Pro Val Gly Ile Ala Ala
 85 90 95
 Gly Phe Asp Lys His Gly Glu Ala Val Asp Gly Leu Tyr Lys Met Gly
 100 105 110
 Phe Gly Phe Val Glu Ile Gly Ser Val Thr Pro Lys Pro Gln Glu Gly
 115 120 125
 Asn Pro Arg Pro Arg Val Phe Arg Leu Pro Glu Asp Gln Ala Val Ile
 130 135 140
 Asn Arg Tyr Gly Phe Asn Ser His Gly Leu Ser Val Val Glu His Arg
 145 150 155 160
 Leu Arg Ala Arg Gln Lys Gln Ala Lys Leu Thr Glu Asp Gly Leu
 165 170 175
 Pro Leu Gly Val Asn Leu Gly Lys Asn Lys Thr Ser Val Asp Ala Ala
 180 185 190
 Glu Asp Tyr Ala Glu Gly Val Arg Val Leu Gly Pro Leu Ala Asp Tyr
 195 200 205
 Leu Val Val Asn Val Ser Ser Pro Asn Thr Ala Gly Leu Arg Ser Leu
 210 215 220
 Gln Gly Lys Ala Glu Leu Arg Arg Leu Leu Thr Lys Val Leu Gln Glu
 225 230 235 240
 Arg Asp Gly Leu Arg Arg Val His Arg Pro Ala Val Leu Val Lys Ile
 245 250 255
 Ala Pro Asp Leu Thr Ser Gln Asp Lys Glu Asp Ile Ala Ser Val Val
 260 265 270
 Lys Glu Leu Gly Ile Asp Gly Leu Ile Val Thr Asn Thr Thr Val Ser
 275 280 285
 Arg Pro Ala Gly Leu Gln Gly Ala Leu Arg Ser Glu Thr Gly Gly Leu
 290 295 300
 Ser Gly Lys Pro Leu Arg Asp Leu Ser Thr Gln Thr Ile Arg Glu Met
 305 310 315 320
 Tyr Ala Leu Thr Gln Gly Arg Val Pro Ile Ile Gly Val Gly Gly Val
 325 330 335
 Ser Ser Gly Gln Asp Ala Leu Glu Lys Ile Arg Ala Gly Ala Ser Leu
 340 345 350
 Val Gln Leu Tyr Thr Ala Leu Thr Phe Trp Gly Pro Pro Val Val Gly
 355 360 365
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214
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 <213> Homo sapien

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 <223> DHODH Truncated 39 kDa Construct

<300>
 <301> Copeland, R.A., et al.
 <302> Recombinant Human Dihydroorotate Dehydrogenase
 <303> Arch. Biochem. Biophys. (1995)
 <304> 323
 <306> 79-86

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 Leu Gln Gly Leu Leu Asp Pro Glu Ser Ala His Arg Leu Ala Val Arg
 20 25 30
 ttc acc tcc ctg ggg ctc ctt cca cgg gcc aga ttt caa gac tct gac 144
 Phe Thr Ser Leu Gly Leu Leu Pro Arg Ala Arg Phe Gln Asp Ser Asp
 35 40 45
 atg ctg gaa gtg aga gtt ctg ggc cat aaa ttc cga aat cca gta gga 192
 Met Leu Glu Val Arg Val Leu Gly His Lys Phe Arg Asn Pro Val Gly
 50 55 60
 att gct gca gga ttt gac aag cat ggg gaa gcc gtg gac gga ctt tat 240
 Ile Ala Ala Gly Phe Asp Lys His Gly Glu Ala Val Asp Gly Leu Tyr
 65 70 75 80
 aag atg ggc ttt ggt ttt gtt gag ata gga agt gtg act cca aaa cct 288
 Lys Met Gly Phe Gly Phe Val Glu Ile Gly Ser Val Thr Pro Lys Pro
 85 90 95
 cag gaa gga aac cct aga ccc aga gtc ttc cgc ctc cct gag gac caa 336
 Gln Glu Gly Asn Pro Arg Pro Arg Val Phe Arg Leu Pro Glu Asp Gln
 100 105 110
 gct gtc att aac agg tat gga ttt aac agt cac ggg ctt tca gtg gtg 384
 Ala Val Ile Asn Arg Tyr Gly Phe Asn Ser His Gly Leu Ser Val Val
 115 120 125
 gaa cac agg tta cgg gcc aga cag cag aag cag gcc aag ctc aca gaa 432
 Glu His Arg Leu Arg Ala Arg Gln Gln Lys Gln Ala Lys Leu Thr Glu
 130 135 140
 gat gga ctg cct ctg ggg gtc aac ttg ggg aag aac aag acc tca gtg 480
 Asp Gly Leu Pro Leu Val Asn Leu Gly Lys Asn Lys Thr Ser Val
 145 150 155 160
 gac gcc gcg gag gac tac gca gaa ggg gtg cgc gta ctg ggc ccc ctg 528
 Asp Ala Ala Glu Asp Tyr Ala Glu Gly Val Arg Val Leu Gly Pro Leu
 165 170 175
 gcc gac tac ctg gtg gtg aat gtg tcc agc ccc aac act gcc ggg ctg 576

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Arg	Ser	Leu	Gln	Gly	Lys	Ala	Glu	Leu	Arg	Arg	Leu	Leu	Thr	Lys	Val		
		195					200					205					
ctg	cag	gag	agg	gat	ggc	ttg	cgg	aga	gtg	cac	agg	ccg	gca	gtc	ctg	672	
Leu	Gln	Glu	Arg	Asp	Gly	Leu	Arg	Arg	Val	His	Arg	Pro	Ala	Val	Leu		
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gtg	aag	atc	gct	cct	gac	ctc	acc	agc	cag	gat	aag	gag	gac	att	gcc	720	
Val	Lys	Ile	Ala	Pro	Asp	Leu	Thr	Ser	Gln	Asp	Lys	Glu	Asp	Ile	Ala		
	225				230					235					240		
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Ser	Val	Val	Lys	Glu	Leu	Gly	Ile	Asp	Gly	Leu	Ile	Val	Thr	Asn	Thr		
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acc	gtg	agt	cgc	cct	gcg	ggc	ctc	cag	ggg	gcc	ctg	cgc	tct	gaa	aca	816	
Thr	Val	Ser	Arg	Pro	Ala	Gly	Leu	Gln	Gly	Ala	Leu	Arg	Ser	Glu	Thr		
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Gly	Gly	Leu	Ser	Gly	Lys	Pro	Leu	Arg	Asp	Leu	Ser	Thr	Gln	Thr	Ile		
		275					280					285					
cgg	gag	atg	tat	gca	ctc	acc	caa	ggc	cga	gtt	ccc	ata	att	ggg	gtt	912	
Arg	Glu	Met	Tyr	Ala	Leu	Thr	Gln	Gly	Arg	Val	Pro	Ile	Ile	Gly	Val		
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Gly	Gly	Val	Ser	Ser	Gly	Gln	Asp	Ala	Leu	Glu	Lys	Ile	Arg	Ala	Gly		
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Ala	Ser	Leu	Val	Gln	Leu	Tyr	Thr	Ala	Leu	Thr	Phe	Trp	Gly	Pro	Pro		
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 35 40 45
 Met Leu Glu Val Arg Val Leu Gly His Lys Phe Arg Asn Pro Val Gly
 50 55 60
 Ile Ala Ala Gly Phe Asp Lys His Gly Glu Ala Val Asp Gly Leu Tyr
 65 70 75 80
 Lys Met Gly Phe Gly Phe Val Glu Ile Gly Ser Val Thr Pro Lys Pro
 85 90 95
 Gln Glu Gly Asn Pro Arg Pro Arg Val Phe Arg Leu Pro Glu Asp Gln

ttc acc tcc ctg ggg ctc ctt cca cgg gcc aga ttt caa gac tct gac	144
Phe Thr Ser Leu Gly Leu Leu Pro Arg Ala Arg Phe Gln Asp Ser Asp	
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atg ctg gaa gtg aga gtt ctg ggc cat aaa ttc cga aat cca gta gga	192
Met Leu Glu Val Arg Val Leu Gly His Lys Phe Arg Asn Pro Val Gly	
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att gct gca gga ttt gac aag cat ggg gaa gcc gtg gac gga ctt tat	240
Ile Ala Ala Gly Phe Asp Lys His Gly Glu Ala Val Asp Gly Leu Tyr	
65 70 75	
aag atg ggc ttt ggt ttt gtt gag ata gga agt gtg act cca aaa cct	288
Lys Met Gly Phe Gly Phe Val Glu Ile Gly Ser Val Thr Pro Lys Pro	
80 85 90 95	
cag gaa gga aac cct aga ccc aga gtc ttc cgc ctc cct gag gac caa	336
Gln Glu Gly Asn Pro Arg Pro Arg Val Phe Arg Leu Pro Glu Asp Gln	
100 105 110	
gct gtc att aac agg tat gga ttt aac agt cac ggg ctt tca gtg gtg	384
Ala Val Ile Asn Arg Tyr Gly Phe Asn Ser His Gly Leu Ser Val Val	
115 120 125	
gaa cac agg tta cgg gcc aga cag cag aag cag gcc aag ctc aca gaa	432
Glu His Arg Leu Arg Ala Arg Gln Gln Lys Gln Ala Lys Leu Thr Glu	
130 135 140	
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Asp Gly Leu Pro Leu Gly Val Asn Leu Gly Lys Asn Lys Thr Ser Val	
145 150 155	
gac gcc gcg gag gac tac gca gaa ggg gtg cgc gta ctg ggc ccc ctg	528
Asp Ala Ala Glu Asp Tyr Ala Glu Gly Val Arg Val Leu Gly Pro Leu	
160 165 170 175	
gcc gac tac ctg gtg gtg aat gtg tcc agc ccc aac act gcc ggg ctg	576
Ala Asp Tyr Leu Val Val Asn Val Ser Ser Pro Asn Thr Ala Gly Leu	
180 185 190	
cgg agc ctt cag gga aag gcc gag ctg cgc cgc ctg ctg acc aag gtg	624
Arg Ser Leu Gln Gly Lys Ala Glu Leu Arg Arg Leu Leu Thr Lys Val	
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ctg cag gag agg gat ggc ttg cgg aga gtg cac agg ccg gca gtc ctg	672
Leu Gln Glu Arg Asp Gly Leu Arg Arg Val His Arg Pro Ala Val Leu	
210 215 220	
gtg aag atc gct cct gac ctc acc agc cag gat aag gag gac att gcc	720
Val Lys Ile Ala Pro Asp Leu Thr Ser Gln Asp Lys Glu Asp Ile Ala	
225 230 235	
agt gtg gtc aaa gag ttg ggc atc gat ggg ctg att gtt acg aac acc	768
Ser Val Val Lys Glu Leu Gly Ile Asp Gly Leu Ile Val Thr Asn Thr	
240 245 250 255	
acc gtg agt cgc cct gcg ggc ctc cag ggt gcc ctg cgc tct gaa aca	816
Thr Val Ser Arg Pro Ala Gly Leu Gln Gly Ala Leu Arg Ser Glu Thr	
260 265 270	
gga ggg ctg agt ggg aag ccc ctc cgg gat tta tca act caa acc att	864
Gly Gly Leu Ser Gly Lys Pro Leu Arg Asp Leu Ser Thr Gln Thr Ile	
275 280 285	
cgg gag atg tat gca ctc acc caa ggc cga gtt ccc ata att ggg gtt	912
Arg Glu Met Tyr Ala Leu Thr Gln Gly Arg Val Pro Ile Ile Gly Val	

290	295	300	
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gcc tcc ctg gtg cag ctg tac acg gcc ctc acc ttc tgg ggg cca ccc Ala Ser Leu Val Gln Leu Tyr Thr Ala Leu Thr Phe Trp Gly Pro Pro 320 325 330 335			1008
gtt gtg ggc aaa gtc aag cgg gaa ctg gag gcc ctt ctg aaa gag cag Val Val Gly Lys Val Lys Arg Glu Leu Glu Ala Leu Leu Lys Glu Gln 340 345 350			1056
ggc ttt ggc gga gtc aca gat gcc att gga gca gat cat cgg agg Gly Phe Gly Gly Val Thr Asp Ala Ile Gly Ala Asp His Arg Arg 355 360 365			1101

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<400> 24

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Thr Ser Leu Gly Leu Leu Pro Arg Ala Arg Phe Gln Asp Ser Asp Met 35 40 45	
Leu Glu Val Arg Val Leu Gly His Lys Phe Arg Asn Pro Val Gly Ile 50 55 60	
Ala Ala Gly Phe Asp Lys His Gly Glu Ala Val Asp Gly Leu Tyr Lys 65 70 75 80	
Met Gly Phe Gly Phe Val Glu Ile Gly Ser Val Thr Pro Lys Pro Gln 85 90 95	
Glu Gly Asn Pro Arg Pro Arg Val Phe Arg Leu Pro Glu Asp Gln Ala 100 105 110	
Val Ile Asn Arg Tyr Gly Phe Asn Ser His Gly Leu Ser Val Val Glu 115 120 125	
His Arg Leu Arg Ala Arg Gln Lys Gln Ala Lys Leu Thr Glu Asp 130 135 140	
Gly Leu Pro Leu Gly Val Asn Leu Gly Lys Asn Lys Thr Ser Val Asp 145 150 155 160	
Ala Ala Glu Asp Tyr Ala Glu Gly Val Arg Val Leu Gly Pro Leu Ala 165 170 175	
Asp Tyr Leu Val Val Asn Val Ser Ser Pro Asn Thr Ala Gly Leu Arg 180 185 190	
Ser Leu Gln Gly Lys Ala Glu Leu Arg Arg Leu Leu Thr Lys Val Leu 195 200 205	
Gln Glu Arg Asp Gly Leu Arg Arg Val His Arg Pro Ala Val Leu Val 210 215 220	
Lys Ile Ala Pro Asp Leu Thr Ser Gln Asp Lys Glu Asp Ile Ala Ser 225 230 235 240	
Val Val Lys Glu Leu Gly Ile Asp Gly Leu Ile Val Thr Asn Thr Thr 245 250 255	
Val Ser Arg Pro Ala Gly Leu Gln Gly Ala Leu Arg Ser Glu Thr Gly 260 265 270	
Gly Leu Ser Gly Lys Pro Leu Arg Asp Leu Ser Thr Gln Thr Ile Arg 275 280 285	
Glu Met Tyr Ala Leu Thr Gln Gly Arg Val Pro Ile Ile Gly Val Gly 290 295 300	
Gly Val Ser Ser Gly Gln Asp Ala Leu Glu Lys Ile Arg Ala Gly Ala 305 310 315 320	
Ser Leu Val Gln Leu Tyr Thr Ala Leu Thr Phe Trp Gly Pro Pro Val 325 330 335	

Val Gly Lys Val Lys Arg Glu Leu Glu Ala Leu Leu Lys Glu Gln Gly
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 Phe Gly Gly Val Thr Asp Ala Ile Gly Ala Asp His Arg Arg
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 <212> DNA
 <213> Aspergillus nidulans

<220>
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 <223> Aspergillus nidulans Val200Glu mutant DHODH cDNA

<221> mutation
 <222> 599
 <223> T to A mutataion

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 Met Ala Thr Asn Ser Phe Arg Lys Leu Thr Phe Ser Gly Ala Ser Arg
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ctg ggt ggt tgt cgc cgt ctc cca cta acc tgc aga caa ctt cga ttc 96
 Leu Gly Gly Cys Arg Arg Leu Pro Leu Thr Cys Arg Gln Leu Arg Phe
 20 25 30

gcc tcc gac agc gga gcc gca gcg gca act aca aaa gca acg gcc gaa 144
 Ala Ser Asp Ser Gly Ala Ala Ala Thr Thr Lys Ala Thr Ala Glu
 35 40 45

tca gca gcc gag tca gct agt ata aac gtc aaa gag gca ccc aaa aag 192
 Ser Ala Ala Glu Ser Ala Ser Ile Asn Val Lys Glu Ala Pro Lys Lys
 50 55 60

gcc gga cgg ggc ctg cgg cgc acg gtc ctg gga acg tcg ttg gcg ctg 240
 Ala Gly Arg Gly Leu Arg Arg Thr Val Leu Gly Thr Ser Leu Ala Leu
 65 70 75 80

acg ctg ctg gtt gga tat gtc tac ggg acg gac acc cgg gcg agt gtg 288
 Thr Leu Leu Val Gly Tyr Val Tyr Gly Thr Asp Thr Arg Ala Ser Val
 85 90 95

cat cgg tac ggt gtt gtg ccg ctg att aga gca ttg tat cct gat gcg 336
 His Arg Tyr Gly Val Val Pro Leu Ile Arg Ala Leu Tyr Pro Asp Ala
 100 105 110

gaa gat gcg cat cat att ggt gtc gat act tta aag atg ctg tat aag 384
 Glu Asp Ala His His Ile Gly Val Asp Thr Leu Lys Met Leu Tyr Lys
 115 120 125

tat ggt ctg cat cca agg gaa cgg ggg gat ccg gat gga gat ggg gcg 432
 Tyr Gly Leu His Pro Arg Glu Arg Gly Asp Pro Asp Gly Asp Gly Ala
 130 135 140

ctg gcg aca gag gtc ttt ggg tat aca ctg tca aac cca att ggc ata 480
 Leu Ala Thr Glu Val Phe Gly Tyr Thr Leu Ser Asn Pro Ile Gly Ile
 145 150 155 160

tcg ggc ggc ctg gac aag cat gct gag atc cct gat ccg ctg ttc gcg 528
 Ser Gly Gly Leu Asp Lys His Ala Glu Ile Pro Asp Pro Leu Phe Ala
 165 170 175

atc ggt cct gcc att gtc gaa gtc ggg ggt acg aca ccc tta cca cag 576
 Ile Gly Pro Ala Ile Val Glu Val Gly Gly Thr Thr Pro Leu Pro Gln
 180 185 190

gat ggt aac ccg cgt cct cgc gaa ttc cga ctt cca tca cag aga gcg Asp Gly Asn Pro Arg Pro Arg Glu Phe Arg Leu Pro Ser Gln Arg Ala 195 200 205	624
atg ata aac cgg tac ggc ctc aac tcc aaa ggc gca gat cac atg gca Met Ile Asn Arg Tyr Gly Leu Asn Ser Lys Gly Ala Asp His Met Ala 210 215 220	672
gct atc ttg gag caa cga gta cgc gat ttt gcc tac gca aac gga ttt Ala Ile Leu Glu Gln Arg Val Arg Asp Phe Ala Tyr Ala Asn Gly Phe 225 230 235 240	720
ggg gca tac gat gcg gct aag cag cgt gta ttg gac ggc gaa gct ggt Gly Ala Tyr Asp Ala Ala Lys Gln Arg Val Leu Asp Gly Glu Ala Gly 245 250 255	768
gtg cca cca ggt agt ctt cag cct ggt aag ctt tta gct gtc caa gtg Val Pro Pro Gly Ser Leu Gln Pro Gly Lys Leu Leu Ala Val Gln Val 260 265 270	816
gca aag aac aag gcc act cct gac ggc gac att gaa gcc atc aag cgc Ala Lys Asn Lys Ala Thr Pro Asp Gly Asp Ile Glu Ala Ile Lys Arg 275 280 285	864
gac tat gtg tat tgc gtg gac cgt gtg gcc aaa tac gct gat att ctt Asp Tyr Val Tyr Cys Val Asp Arg Val Ala Lys Tyr Ala Asp Ile Leu 290 295 300	912
gtt gtg aat gta tcg agc ccc aac aca ccc ggt ctc cgt gac ctt caa Val Val Asn Val Ser Ser Pro Asn Thr Pro Gly Leu Arg Asp Leu Gln 305 310 315 320	960
gcc act gcc ccg ctc aca gct atc ttg agt gct gtc gtt ggc gcg gca Ala Thr Ala Pro Leu Thr Ala Ile Leu Ser Ala Val Val Gly Ala Ala 325 330 335	1008
aag agc gtg aac cgc aag acc aaa cca tat gtt atg gtc aag gtc agt Lys Ser Val Asn Arg Lys Thr Lys Pro Tyr Val Met Val Lys Val Ser 340 345 350	1056
ccg gat gaa gac tca gat gaa caa gtc tct ggt atc tgc gac gcc gtc Pro Asp Glu Asp Ser Asp Glu Gln Val Ser Gly Ile Cys Asp Ala Val 355 360 365	1104
cga gca tcc ggt gtc gac gga gtg att gtc gga aac aca aca aac cgt Arg Ala Ser Gly Val Asp Gly Val Ile Val Gly Asn Thr Thr Asn Arg 370 375 380	1152
cgc ccc gac cct ata ccc caa ggt tac act ctt ccg gcc aag gag cag Arg Pro Asp Pro Ile Pro Gln Gly Tyr Thr Leu Pro Ala Lys Glu Gln 385 390 395 400	1200
gca acg ttg aaa gaa acc ggc ggg tat tca ggt cca cag ctg ttc gat Ala Thr Leu Lys Glu Thr Gly Gly Tyr Ser Gly Pro Gln Leu Phe Asp 405 410 415	1248
cgc aca gtg gcc ctt gtg gct cgg tac cgc tcc atg ctg gat gcg gag Arg Thr Val Ala Leu Val Ala Arg Tyr Arg Ser Met Leu Asp Ala Glu 420 425 430	1296
tcg gaa acg gcc gga tcc gcc aag gat tca gca gcg acc ata gcg caa Ser Glu Thr Ala Gly Ser Ala Lys Asp Ser Ala Ala Thr Ile Ala Gln 435 440 445	1344
aca gag cca ggc tcg gaa aac gtt cct cct gtg gaa gcg cca agc gga Thr Glu Pro Gly Ser Glu Asn Val Pro Pro Val Glu Ala Pro Ser Gly	1392

450	455	460	
ctg ccg cgc aaa gtt atc ttc gct tgc ggt ggt atc acc aac ggg aag			1440
Leu Pro Arg Lys Val Ile Phe Ala Ser Gly Gly Ile Thr Asn Gly Lys			
465	470	475	480
cag gct cac gct gtt tta gac aca ggg gca tct gtt gcc atg atg tac			1488
Gln Ala His Ala Val Leu Asp Thr Gly Ala Ser Val Ala Met Met Tyr			
	485	490	495
acc ggt gtg gtc tat ggt ggc gtc ggc act gtc act cga gtg aag caa			1536
Thr Gly Val Val Tyr Gly Gly Val Gly Thr Val Thr Arg Val Lys Gln			
	500	505	510
gaa ctt cga acg gcg aaa aag gag			1560
Glu Leu Arg Thr Ala Lys Lys Glu			
	515	520	

<210> 26
 <211> 520
 <212> PRT
 <213> *Aspergillus nidulans*

<400> 26

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			20					25				30			
Ala	Ser	Asp	Ser	Gly	Ala	Ala	Ala	Ala	Thr	Thr	Lys	Ala	Thr	Ala	Glu
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Ser	Ala	Ala	Glu	Ser	Ala	Ser	Ile	Asn	Val	Lys	Glu	Ala	Pro	Lys	Lys
	50					55					60				
Ala	Gly	Arg	Gly	Leu	Arg	Arg	Thr	Val	Leu	Gly	Thr	Ser	Leu	Ala	Leu
65					70					75					80
Thr	Leu	Leu	Val	Gly	Tyr	Val	Tyr	Gly	Thr	Asp	Thr	Arg	Ala	Ser	Val
			85						90					95	
His	Arg	Tyr	Gly	Val	Val	Pro	Leu	Ile	Arg	Ala	Leu	Tyr	Pro	Asp	Ala
			100					105					110		
Glu	Asp	Ala	His	His	Ile	Gly	Val	Asp	Thr	Leu	Lys	Met	Leu	Tyr	Lys
		115					120					125			
Tyr	Gly	Leu	His	Pro	Arg	Glu	Arg	Gly	Asp	Pro	Asp	Gly	Asp	Gly	Ala
	130					135					140				
Leu	Ala	Thr	Glu	Val	Phe	Gly	Tyr	Thr	Leu	Ser	Asn	Pro	Ile	Gly	Ile
145					150					155					160
Ser	Gly	Gly	Leu	Asp	Lys	His	Ala	Glu	Ile	Pro	Asp	Pro	Leu	Phe	Ala
			165					170						175	
Ile	Gly	Pro	Ala	Ile	Val	Glu	Val	Gly	Gly	Thr	Thr	Pro	Leu	Pro	Gln
			180					185					190		
Asp	Gly	Asn	Pro	Arg	Pro	Arg	Glu	Phe	Arg	Leu	Pro	Ser	Gln	Arg	Ala
		195					200					205			
Met	Ile	Asn	Arg	Tyr	Gly	Leu	Asn	Ser	Lys	Gly	Ala	Asp	His	Met	Ala
	210					215					220				
Ala	Ile	Leu	Glu	Gln	Arg	Val	Arg	Asp	Phe	Ala	Tyr	Ala	Asn	Gly	Phe
225					230					235					240
Gly	Ala	Tyr	Asp	Ala	Ala	Lys	Gln	Arg	Val	Leu	Asp	Gly	Glu	Ala	Gly
			245						250					255	
Val	Pro	Pro	Gly	Ser	Leu	Gln	Pro	Gly	Lys	Leu	Leu	Ala	Val	Gln	Val
			260					265					270		
Ala	Lys	Asn	Lys	Ala	Thr	Pro	Asp	Gly	Asp	Ile	Glu	Ala	Ile	Lys	Arg
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	290					295					300				
Val	Val	Asn	Val	Ser	Ser	Pro	Asn	Thr	Pro	Gly	Leu	Arg	Asp	Leu	Gln
305					310					315					320
Ala	Thr	Ala	Pro	Leu	Thr	Ala	Ile	Leu	Ser	Ala	Val	Val	Gly	Ala	Ala
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gaa gat gtg cat cat att ggt gtc gat act tta aag atg ctg tat aag Glu Asp Val His His Ile Gly Val Asp Thr Leu Lys Met Leu Tyr Lys 115 120 125	384
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ctg gcg aca gag gtc ttt ggg tat aca ctg tca aac cca att ggc ata Leu Ala Thr Glu Val Phe Gly Tyr Thr Leu Ser Asn Pro Ile Gly Ile 145 150 155 160	480
tcg ggc ggc ctg gac aag cat gct gag atc cct gat ccg ctg ttc gcg Ser Gly Gly Leu Asp Lys His Ala Glu Ile Pro Asp Pro Leu Phe Ala 165 170 175	528
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gat ggt aac ccg cgt cct cgc gta ttc cga ctt cca tca cag aga gcg Asp Gly Asn Pro Arg Pro Arg Val Phe Arg Leu Pro Ser Gln Arg Ala 195 200 205	624
atg ata aac ccg tac ggc ctc aac tcc aaa ggc gca gat cac atg gca Met Ile Asn Arg Tyr Gly Leu Asn Ser Lys Gly Ala Asp His Met Ala 210 215 220	672
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gac tat gtg tat tgc gtg gac cgt gtg gcc aaa tac gct gat att ctt Asp Tyr Val Tyr Cys Val Asp Arg Val Ala Lys Tyr Ala Asp Ile Leu 290 295 300	912
gtt gtg aat gta tcg agc ccc aac aca ccc ggt ctc cgt gac ctt caa Val Val Asn Val Ser Pro Asn Thr Pro Gly Leu Arg Asp Leu Gln 305 310 315 320	960
gcc act gcc ccg ctc aca gct atc ttg agt gct gtc gtt ggc gcg gca Ala Thr Ala Pro Leu Thr Ala Ile Leu Ser Ala Val Val Gly Ala Ala 325 330 335	1008
aag agc gtg aac cgc aag acc aaa cca tat gtt atg gtc aag gtc agt Lys Ser Val Asn Arg Lys Thr Lys Pro Tyr Val Met Val Lys Val Ser 340 345 350	1056
ccg gat gaa gac tca gat gaa caa gtc tct ggt atc tgc gac gcc gtc Pro Asp Glu Asp Ser Asp Glu Gln Val Ser Gly Ile Cys Asp Ala Val 355 360 365	1104
cga gca tcc ggt gtc gac gga gtg att gtc gga aac aca aca aac cgt Arg Ala Ser Gly Val Asp Gly Val Ile Val Gly Asn Thr Thr Asn Arg	1152

370	375	380	
cgc ccc gac cct ata ccc caa ggt tac act ctt ccg gcc aag gag cag Arg Pro Asp Pro Ile Pro Gln Gly Tyr Thr Leu Pro Ala Lys Glu Gln 385 390 395 400			1200
gca acg ttg aaa gaa acc ggc ggg tat tca ggt cca cag ctg ttc gat Ala Thr Leu Lys Glu Thr Gly Gly Tyr Ser Gly Pro Gln Leu Phe Asp 405 410 415			1248
cgc aca gtg gcc ctt gtg gct cgg tac cgc tcc atg ctg gat gcg gag Arg Thr Val Ala Leu Val Ala Arg Tyr Arg Ser Met Leu Asp Ala Glu 420 425 430			1296
tcg gaa acg gcc gga tcc gcc aag gat tca gca gcg acc ata gcg caa Ser Glu Thr Ala Gly Ser Ala Lys Asp Ser Ala Ala Thr Ile Ala Gln 435 440 445			1344
aca gag cca ggc tcg gaa aac gtt cct cct gtg gaa gcg cca agc gga Thr Glu Pro Gly Ser Glu Asn Val Pro Pro Val Glu Ala Pro Ser Gly 450 455 460			1392
ctg ccg cgc aaa gtt atc ttc gct tcg ggt ggt atc acc aac ggg aag Leu Pro Arg Lys Val Ile Phe Ala Ser Gly Gly Ile Thr Asn Gly Lys 465 470 475 480			1440
cag gct cac gct gtt tta gac aca ggg gca tct gtt gcc atg atg tac Gln Ala His Ala Val Leu Asp Thr Gly Ala Ser Val Ala Met Met Tyr 485 490 495			1488
acc ggt gtg gtc tat ggt ggc gtc ggc act gtc act cga gtg aag caa Thr Gly Val Val Tyr Gly Gly Val Gly Thr Val Thr Arg Val Lys Gln 500 505 510			1536
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<210> 28
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 <212> PRT
 <213> Aspergillus nidulans

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 35 40 45
 Ser Ala Ala Glu Ser Ala Ser Ile Asn Val Lys Glu Ala Pro Lys Lys
 50 55 60
 Ala Gly Arg Gly Leu Arg Arg Thr Val Leu Gly Thr Ser Leu Ala Leu
 65 70 75 80
 Thr Leu Leu Val Gly Tyr Val Tyr Gly Thr Asp Thr Arg Ala Ser Val
 85 90 95
 His Arg Tyr Gly Val Val Pro Leu Ile Arg Ala Leu Tyr Pro Asp Ala
 100 105 110
 Glu Asp Val His His Ile Gly Val Asp Thr Leu Lys Met Leu Tyr Lys
 115 120 125
 Tyr Gly Leu His Pro Arg Glu Arg Gly Asp Pro Asp Gly Asp Gly Ala
 130 135 140
 Leu Ala Thr Glu Val Phe Gly Tyr Thr Leu Ser Asn Pro Ile Gly Ile
 145 150 155 160
 Ser Gly Gly Leu Asp Lys His Ala Glu Ile Pro Asp Pro Leu Phe Ala
 165 170 175

Ile Gly Pro Ala Ile Val Glu Val Gly Gly Thr Thr Pro Leu Pro Gln
 180 185 190
 Asp Gly Asn Pro Arg Pro Arg Val Phe Arg Leu Pro Ser Gln Arg Ala
 195 200 205
 Met Ile Asn Arg Tyr Gly Leu Asn Ser Lys Gly Ala Asp His Met Ala
 210 215 220
 Ala Ile Leu Glu Gln Arg Val Arg Asp Phe Ala Tyr Ala Asn Gly Phe
 225 230 235 240
 Gly Ala Tyr Asp Ala Ala Lys Gln Arg Val Leu Asp Gly Glu Ala Gly
 245 250 255
 Val Pro Pro Gly Ser Leu Gln Pro Gly Lys Leu Leu Ala Val Gln Val
 260 265 270
 Ala Lys Asn Lys Ala Thr Pro Asp Gly Asp Ile Glu Ala Ile Lys Arg
 275 280 285
 Asp Tyr Val Tyr Cys Val Asp Arg Val Ala Lys Tyr Ala Asp Ile Leu
 290 295 300
 Val Val Asn Val Ser Ser Pro Asn Thr Pro Gly Leu Arg Asp Leu Gln
 305 310 315 320
 Ala Thr Ala Pro Leu Thr Ala Ile Leu Ser Ala Val Val Gly Ala Ala
 325 330 335
 Lys Ser Val Asn Arg Lys Thr Lys Pro Tyr Val Met Val Lys Val Ser
 340 345 350
 Pro Asp Glu Asp Ser Asp Glu Gln Val Ser Gly Ile Cys Asp Ala Val
 355 360 365

Arg Ala Ser Gly Val Asp Gly Val Ile Val Gly Asn Thr Thr Asn Arg
 370 375 380
 Arg Pro Asp Pro Ile Pro Gln Gly Tyr Thr Leu Pro Ala Lys Glu Gln
 385 390 395 400
 Ala Thr Leu Lys Glu Thr Gly Gly Tyr Ser Gly Pro Gln Leu Phe Asp
 405 410 415
 Arg Thr Val Ala Leu Val Ala Arg Tyr Arg Ser Met Leu Asp Ala Glu
 420 425 430
 Ser Glu Thr Ala Gly Ser Ala Lys Asp Ser Ala Ala Thr Ile Ala Gln
 435 440 445
 Thr Glu Pro Gly Ser Glu Asn Val Pro Pro Val Glu Ala Pro Ser Gly
 450 455 460
 Leu Pro Arg Lys Val Ile Phe Ala Ser Gly Gly Ile Thr Asn Gly Lys
 465 470 475 480
 Gln Ala His Ala Val Leu Asp Thr Gly Ala Ser Val Ala Met Met Tyr
 485 490 495
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 515 520

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<220>
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 Met Ala Asp Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro
 1 5 10
 gac gac ggg ctc aca gcg cag cag ctc ttc aac tgc ggg gac ggc ctc 156
 Asp Asp Gly Leu Thr Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu
 15 20 25 30
 acc tac aat gat ttt ctc att ctt cct ggg tat atc gac ttc act gca 204
 Thr Tyr Asn Asp Phe Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala

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Asp	Gln	Val	Asp	Leu	Thr	Ser	Ala	Leu	Thr	Lys	Lys	Ile	Thr	Leu	Lys					
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acc	cca	ttg	gtt	tcc	tca	ccc	atg	gac	act	gtc	aca	gag	gct	gga	atg	300				
Thr	Pro	Leu	Val	Ser	Ser	Pro	Met	Asp	Thr	Val	Thr	Glu	Ala	Gly	Met					
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gcc	atc	gcg	atg	gcg	ctt	aca	gga	ggg	att	ggg	ttc	atc	cac	cac	aac	348				
Ala	Ile	Ala	Met	Ala	Leu	Thr	Gly	Gly	Ile	Gly	Phe	Ile	His	His	Asn					
	80					85					90									
tgc	aca	cct	gaa	ttc	cag	gcc	aat	gaa	gtt	cgg	aaa	gtg	aag	aaa	tac	396				
Cys	Thr	Pro	Glu	Phe	Gln	Ala	Asn	Glu	Val	Arg	Lys	Val	Lys	Lys	Tyr					
	95				100					105					110					
gaa	cag	gga	ttc	atc	act	gac	ccc	gtg	gtc	ctt	agc	ccc	aag	gat	cgt	444				
Glu	Gln	Gly	Phe	Ile	Thr	Asp	Pro	Val	Val	Leu	Ser	Pro	Lys	Asp	Arg					
				115					120					125						
gta	cgc	gat	gtt	ttt	gag	gcc	aaa	gcc	agg	cat	ggc	ttc	tgt	ggg	atc	492				
Val	Arg	Asp	Val	Phe	Glu	Ala	Lys	Ala	Arg	His	Gly	Phe	Cys	Gly	Ile					
			130					135					140							
ccc	atc	aca	gat	aca	ggc	cgg	atg	ggg	agt	cga	ttg	gtg	ggc	atc	atc	540				
Pro	Ile	Thr	Asp	Thr	Gly	Arg	Met	Gly	Ser	Arg	Leu	Val	Gly	Ile	Ile					
		145					150					155								
tcc	tca	agg	gac	att	gat	ttc	ctc	aag	gag	gaa	gag	cat	gac	cgg	ttc	588				
Ser	Ser	Arg	Asp	Ile	Asp	Phe	Leu	Lys	Glu	Glu	Glu	His	Asp	Arg	Phe					
	160					165					170									
ttg	gaa	gag	atc	atg	act	aag	agg	gaa	gat	ttg	gtg	gtc	gcc	cct	gcc	636				
Leu	Glu	Glu	Ile	Met	Thr	Lys	Arg	Glu	Asp	Leu	Val	Val	Ala	Pro	Ala					
	175				180				185						190					
ggc	gtc	act	ctg	aaa	gag	gca	aat	gag	att	ctg	cag	cga	agt	aaa	aag	684				
Gly	Val	Thr	Leu	Lys	Glu	Ala	Asn	Glu	Ile	Leu	Gln	Arg	Ser	Lys	Lys					
			195					200						205						
gga	aag	ttg	ccc	att	gtg	aat	gaa	aat	gat	gag	ctg	gta	gcc	atc	att	732				
Gly	Lys	Leu	Pro	Ile	Val	Asn	Glu	Asn	Asp	Glu	Leu	Val	Ala	Ile	Ile					
		210					215						220							
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Ala	Arg	Thr	Asp	Leu	Lys	Lys	Asn	Arg	Asp	Tyr	Pro	Leu	Ala	Ser	Lys					
		225					230					235								
gat	gcc	aag	aag	caa	ctg	ctg	tgt	ggg	gca	gcc	att	ggc	act	cat	gag	828				
Asp	Ala	Lys	Lys	Gln	Leu	Leu	Cys	Gly	Ala	Ala	Ile	Gly	Thr	His	Glu					
	240				245						250									
gat	gac	aag	tat	agg	ctg	gac	tta	ctg	gcc	ctt	gct	ggg	gtg	gat	gta	876				
Asp	Asp	Lys	Tyr	Arg	Leu	Asp	Leu	Leu	Ala	Leu	Ala	Gly	Val	Asp	Val					
	255				260					265					270					
gtg	gtt	ttg	gac	tct	tcc	cag	gga	aac	tcc	atc	ttc	caa	atc	aat	atg	924				
Val	Val	Leu	Asp	Ser	Ser	Gln	Gly	Asn	Ser	Ile	Phe	Gln	Ile	Asn	Met					
			275						280					285						
atc	aaa	tac	atc	aag	gag	aag	tat	ccc	agt	cta	cag	gtc	att	gga	ggc	972				
Ile	Lys	Tyr	Ile	Lys	Glu	Lys	Tyr	Pro	Ser	Leu	Gln	Val	Ile	Gly	Gly					
		290						295					300							
aat	gta	gtc	act	gct	gcg	caa	gcc	aag	aac	ctc	ata	gat	gca	ggg	gta	1020				

Asn	Val	Val	Thr	Ala	Ala	Gln	Ala	Lys	Asn	Leu	Ile	Asp	Ala	Gly	Val		
		305					310					315					
gat	gct	ttg	cga	gtc	ggc	atg	gga	agt	ggg	tcc	atc	tgc	atc	acc	cag		1068
Asp	Ala	Leu	Arg	Val	Gly	Met	Gly	Ser	Gly	Ser	Ile	Cys	Ile	Thr	Gln		
		320				325					330						
gaa	gtg	ttg	gcc	tgt	ggg	cgg	ccc	caa	gcc	aca	gca	gtg	tac	aag	gtc		1116
Glu	Val	Leu	Ala	Cys	Gly	Arg	Pro	Gln	Ala	Thr	Ala	Val	Tyr	Lys	Val		
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Ser	Glu	Tyr	Ala	Arg	Arg	Phe	Gly	Val	Pro	Val	Ile	Ala	Asp	Gly	Gly		
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Ile	Gln	Asn	Val	Gly	His	Ile	Ala	Lys	Ala	Leu	Ala	Leu	Gly	Ala	Ser		
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Thr	Val	Met	Met	Gly	Ser	Leu	Leu	Ala	Ala	Thr	Thr	Glu	Ala	Pro	Gly		
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Glu	Tyr	Phe	Phe	Ser	Asp	Gly	Ile	Arg	Leu	Lys	Lys	Tyr	Arg	Gly	Met		
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Gly	Ser	Leu	Asp	Ala	Met	Asp	Lys	His	Leu	Ser	Ser	Gln	Asn	Arg	Tyr		
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Phe	Ser	Glu	Ala	Asp	Lys	Ile	Lys	Val	Ala	Gln	Gly	Val	Ser	Gly	Ala		
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Val	Gln	Asp	Lys	Gly	Ser	Ile	His	Lys	Phe	Val	Pro	Tyr	Leu	Ile	Ala		
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Val	Arg	Ala	Met	Thr	Tyr	Ser	Gly	Glu	Leu	Lys	Phe	Glu	Lys	Arg	Thr		
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Ser	Ser	Ala	Gln	Val	Glu	Gly	Gly	Val	His	Ser	Leu	His	Ser	Tyr	Glu		
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aaa	cgg	ctt	ttc	tga	aaacagatcc	agtatatgcc	ttgaattttt	caataaaagt									1651
Lys	Arg	Leu	Phe	*													

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 <212> PRT
 <213> Mus musculus

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Arg	Asp	Ile	Asp	Phe	Leu	Lys	Glu	Glu	Glu	His	Asp	Arg	Phe	Leu	Glu
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 <213> Mus musculus

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	400					405					410									
ggg	tct	ctt	gat	gcc	atg	gac	aaa	cat	ctc	agc	agc	cag	aac	cga	tac	1356				
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Phe	Ser	Glu	Ala	Asp	Lys	Ile	Lys	Val	Ala	Gln	Gly	Val	Ser	Gly	Ala					
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gtg	cag	gac	aag	ggg	tct	atc	cac	aag	ttc	gtt	cct	tac	ctg	att	gct	1452				
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Val Arg Ala Met Thr Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr
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tcc tct gct cag gtg gaa ggt ggc gtc cac agc ctc cat tcg tac gag 1596
Ser Ser Ala Gln Val Glu Gly Gly Val His Ser Leu His Ser Tyr Glu
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<210> 32
<211> 514
<212> PRT
<213> Mus musculus

<400> 32

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35 40 45
Val Asp Leu Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro
50 55 60
Leu Val Ser Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met Ala Ile
65 70 75 80
Ala Met Ala Leu Thr Gly Gly Ile Gly Phe Ile His His Asn Cys Thr
85 90 95
Pro Glu Phe Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr Glu Gln
100 105 110
Gly Phe Ile Thr Asp Pro Val Val Leu Ser Pro Lys Asp Arg Val Arg
115 120 125
Asp Val Phe Glu Ala Lys Ala Arg His Gly Phe Cys Gly Ile Pro Ile
130 135 140
Thr Asp Thr Gly Arg Met Gly Ser Arg Leu Val Gly Ile Ile Ser Ser
145 150 155 160
Arg Asp Ile Asp Phe Leu Lys Glu Glu Glu His Asp Arg Phe Leu Glu
165 170 175
Glu Ile Met Thr Lys Arg Glu Asp Leu Val Val Ala Pro Ala Gly Val
180 185 190
Thr Leu Lys Glu Ala Asn Glu Ile Leu Gln Arg Ser Lys Lys Gly Lys
195 200 205
Leu Pro Ile Val Asn Glu Asn Asp Glu Leu Val Ala Ile Ile Ala Arg
210 215 220
Thr Asp Leu Lys Lys Asn Arg Asp Tyr Pro Leu Ala Ser Lys Asp Ala
225 230 235 240
Lys Lys Gln Leu Leu Cys Gly Ala Ala Ile Gly Thr His Glu Asp Asp
245 250 255
Lys Tyr Arg Leu Asp Leu Leu Ala Leu Ala Gly Val Asp Val Val Val
260 265 270
Leu Asp Ser Ser Gln Gly Asn Ser Ile Phe Gln Ile Asn Met Ile Lys
275 280 285
Tyr Ile Lys Glu Lys Tyr Pro Ser Leu Gln Val Ile Gly Gly Asn Val
290 295 300
Val Thr Ala Ala Gln Ala Lys Asn Leu Ile Asp Ala Gly Val Asp Ala
305 310 315 320
Leu Arg Val Gly Met Gly Ser Gly Ser Ile Cys Ile Ile Gln Glu Val
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Leu Ala Cys Gly Arg Pro Gln Ala Thr Ala Val Tyr Lys Val Tyr Glu
340 345 350

Tyr Ala Arg Arg Phe Gly Val Pro Val Ile Ala Asp Gly Gly Ile Gln
 355 360 365
 Asn Val Gly His Ile Ala Lys Ala Leu Ala Leu Gly Ala Ser Thr Val
 370 375 380
 Met Met Gly Ser Leu Leu Ala Ala Thr Thr Glu Ala Pro Gly Glu Tyr
 385 390 395 400
 Phe Phe Ser Asp Gly Ile Arg Leu Lys Lys Tyr Arg Gly Met Gly Ser
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 Glu Ala Asp Lys Ile Lys Val Ala Gln Gly Val Ser Gly Ala Val Gln
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 Asp Lys Gly Ser Ile His Lys Phe Val Pro Tyr Leu Ile Ala Gly Ile
 450 455 460
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<210> 33

<211> 5627

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Sequence of pMG
plasmid from InvivoGen

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